

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/670,106

DATE: 05/14/2001  
TIME: 11:35:06

Input Set : N:\Crf3\RULE60\09670106.txt  
Output Set: N:\CRF3\05142001\I670106.raw

## SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:  
6 (i) APPLICANT: BLACK, ROY A  
7 SLEATH, PAUL R  
8 KRONHEIM, SHIRLEY R  
10 (ii) TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
11 INTERLEUKIN 1B PROTEASE INHIBITORS  
14 (iii) NUMBER OF SEQUENCES: 24  
16 (iv) CORRESPONDENCE ADDRESS:  
17 (A) ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
18 MILNAMOW  
20 (B) STREET: 180 N. STETSON  
21 (C) CITY: CHICAGO  
22 (D) STATE: IL  
23 (E) COUNTRY: USA  
24 (F) ZIP: 60601  
26 (v) COMPUTER READABLE FORM:  
27 (A) MEDIUM TYPE: Floppy disk  
28 (B) COMPUTER: IBM PC compatible  
29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
30 (D) SOFTWARE: PatentIn Release #1.24  
32 (vi) CURRENT APPLICATION DATA:  
C--> 33 (A) APPLICATION NUMBER: US/09/670,106  
C--> 34 (B) FILING DATE: 26-Sep-2000  
36 (vii) PRIOR APPLICATION DATA:  
37 (A) APPLICATION NUMBER: US/08/203,716  
38 (B) FILING DATE: 08-FEB-1994  
39 (A) APPLICATION NUMBER: US/07/750,644  
40 (B) FILING DATE:  
42 (viii) ATTORNEY/AGENT INFORMATION:  
43 (A) NAME: KATZ, MARTIN L.  
44 (B) REGISTRATION NUMBER: 25011  
45 (C) REFERENCE/DOCKET NUMBER: IMMUNEX2108  
47 (ix) TELECOMMUNICATION INFORMATION:  
48 (A) TELEPHONE: 3126165400  
49 (B) TELEFAX: 3126165460  
50 (C) TELEX: 9102211206  
53 (2) INFORMATION FOR SEQ ID NO: 1:  
55 (i) SEQUENCE CHARACTERISTICS:  
56 (A) LENGTH: 1659 base pairs  
57 (B) TYPE: nucleic acid  
58 (C) STRANDEDNESS: single  
59 (D) TOPOLOGY: linear  
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
62 AAAAGGAGAG AAAAGCCTAA AAGAGAGTGG GTAGATGGCC GACAAGGTCC TGAAGGAGAA 60  
64 GAGAAAGCTG TTTATCCGTT CCATGGGTGA AGGTACAATA AATGGCTTAA GGTAGAAGGT 120  
66 GAAGGAAATA CTGGATGAAT TATTACAGAC AAGGGTGCTG AACAAAGGAAG AGATGGAGAA 180

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68	AGTAAAACGT	GAAAATGCTA	CAGTTTATAG	AAAAGAAGAA	CGCTTATGGA	TAAGACCCGA	240
70	GCTTGATTG	ACTCCGTTAT	TCCGAAAGGG	GCACAGGCAT	GCCAAATTG	CATCACATAC	300
72	CGGATAAGTC	AAAGTGATAA	TTTGTGAAGA	AGACAGTTAC	CTGGCAGGGA	CGCTGGGACT	360
74	CTCAGCAGAT	CAAACATCTG	GAAATTACCT	TAATTGAGGA	AAGAAAGAAA	ATTATGCAAG	420
76	ACTCTCAAGG	AGTACTTTCT	TCCTTCCAG	CTCCTCAGGC	AGTGCAGGAC	AACCCAGCTA	480
78	TGCCACAGG	GAACGGAAGA	GTGAATCCTC	AGGCTCAGAA	GGGAATGTCA	AGCTTTGCTC	540
80	CCTAGAAGAA	GCTCAAAGGA	TATGGAAACA	AAAGTCGGCA	GTAAAGTAGA	ACAGGAGAGA	600
82	TTTATCCAAT	AATGGACAAG	TCAAGCCGCA	CACGTCTTGC	TCTCATTATC	TGCAATGAAG	660
84	AATTGACAG	TAGAGTGAAG	AATGTTTGAG	TAATTCTTAG	AAGAACTGGA	GCTGAGGTTG	720
86	ACATCACAGG	CATGACAATG	CTGCTACAAA	ATCTGGGGTA	CAGCGTAAA	TAAATTGGA	780
88	AAAAGGGATG	TGAAAAAAA	TCTCACTGCT	TCGGACATGA	CTACAGAGCT	GGAGGCATT	840
90	GCACACCGCC	CAGAGCACAA	GTATATGAGG	CGGGACCTCT	GACAGCACGT	TCCTGGTGT	900
92	CATGTCTCAT	GGTATTGGG	AAGGCATTG	TGGGAAGAAA	CACTCTGAGG	AAGAAAATAT	960
94	ACACAAGTCC	CAGATATACT	ACAACCTAAC	GCAATTTA	ACATGTTGAA	TACCAAGAAC	1020
96	TGCCCAAGTT	TGAAGGACAG	AACAGGAGAA	TAAGAAACCG	AAGGTGATCA	TCATCCAGGC	1080
98	CTGCCGTGGT	GACAGCCCTG	GTGTGGTGTG	GTAAAGAT	TCAGTAGGAA	GATTGGGAAA	1140
100	AAAGGTTCT	GGAAACCTAT	CTTTACCAAC	TACAGAAGAG	TTTGAGGATG	ATGCTATTAA	1200
102	GAAAGCCAC	ATAGAGAAGA	AACTAAATAG	TTGAGATTT	ATCGCTTCT	GCTCTTCCAC	1260
104	ACCAAGATAAT	GTTCCTTGG	GACATCCCAC	AATGGGCTCT	GTTCCTTATTG	AGGTGGTAAC	1320
106	CAAGGAGAAAG	GGAAAGACTCA	TTGAACATAT	GCAAGAATAT	GCCTGTTCT	GTGATGTGGA	1380
108	GGAAATTTC	CGCAAGGTT	GATTTGGAGA	GAAGTTTGAG	ATTAGCTCA	TTTGAGCAGC	1440
110	CAGATGGTAG	AGCGCAGATG	CCCACCACTG	AAAGAGTGAC	TTTGACAAGA	TGTTTCTACC	1500
112	TCGTTCCCAG	GACATTTAAA	TAAGGAAACT	GTATGAATGT	CTGCGGGCAG	GAAGTGAAGA	1560
114	GATCGTTCTG	TAAGGTTT	TTGGAATTAT	GTCTGCTGAA	TAATAAACTT	TTTTGAAAT	1620
116	AATAAATCTG	GTAGAAAAAT	AAAAAAAAAA	AAAAAAAAAA			1659

121 (2) INFORMATION FOR SEQ ID NO: 2:

123 (i) SEQUENCE CHARACTERISTICS:  
124 (A) LENGTH: 404 amino acids  
125 (B) TYPE: amino acid  
126 (D) TOPOLOGY: linear

127 (ii) MOLECULE TYPE: peptide

129 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

131	Met	Ala	Asp	Lys	Val	Leu	Lys	Glu	Lys	Arg	Lys	Leu	Phe	Ile	Arg	Ser	
132	1				5				10					15			
134	Met	Gly	Glu	Gly	Thr	Ile	Asn	Gly	Leu	Leu	Asp	Glu	Leu	Leu	Gln	Thr	
135					20				25					30			
137	Arg	Val	Leu	Asn	Lys	Glu	Glu	Met	Glu	Lys	Val	Lys	Arg	Glu	Asn	Ala	
138					35				40					45			
140	Thr	Val	Met	Asp	Lys	Thr	Arg	Ala	Leu	Ile	Asp	Ser	Val	Ile	Pro	Lys	
141					50				55					60			
143	Gly	Ala	Gln	Ala	Cys	Gln	Ile	Cys	Ile	Thr	Tyr	Ile	Cys	Glu	Glu	Asp	
144					65				70					75			80
146	Ser	Tyr	Leu	Ala	Gly	Thr	Leu	Gly	Leu	Ser	Ala	Asp	Gln	Thr	Ser	Gly	
147					85				90					95			
149	Asn	Tyr	Leu	Asn	Met	Gln	Asp	Ser	Gln	Gly	Val	Leu	Ser	Ser	Phe	Pro	
150					100				105					110			
152	Ala	Pro	Gln	Ala	Val	Gln	Asp	Asn	Pro	Ala	Met	Pro	Thr	Ser	Ser	Gly	
153					115				120					125			
155	Ser	Glu	Gly	Asn	Val	Lys	Leu	Cys	Ser	Leu	Glu	Ala	Gln	Arg	Ile		

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156 130 135 140  
158 Trp Lys Gln Lys Ser Ala Glu Ile Tyr Pro Ile Met Asp Lys Ser Ser  
159 145 150 155 160  
161 Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Glu Glu Phe Asp Ser Ile  
162 165 170 175  
164 Pro Arg Arg Thr Gly Ala Glu Val Asp Ile Thr Gly Met Thr Met Leu  
165 180 185 190  
167 Leu Gln Asn Leu Gly Tyr Ser Val Asp Val Lys Lys Asn Leu Thr Ala  
168 195 200 205  
170 Ser Asp Met Thr Thr Glu Leu Glu Ala Phe Ala His Arg Pro Glu His  
171 210 215 220  
173 Lys Thr Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Arg  
174 225 230 235 240  
176 Glu Gly Ile Cys Gly Lys Lys His Ser Glu Gln Val Pro Asp Ile Leu  
177 245 250 255  
179 Gln Leu Asn Ala Ile Phe Asn Met Leu Asn Thr Lys Asn Cys Pro Ser  
180 260 265 270  
182 Leu Lys Asp Lys Pro Lys Val Ile Ile Ile Gln Ala Cys Arg Gly Asp  
183 275 280 285  
185 Ser Pro Gly Val Val Trp Phe Lys Asp Ser Val Gly Val Ser Gly Asn  
186 290 295 300  
188 Leu Ser Leu Pro Thr Thr Glu Glu Phe Asp Asp Ala Ile Lys Lys  
189 305 310 315 320  
191 Ala His Ile Glu Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr Pro Asp  
192 325 330 335  
194 Asn Val Ser Trp Arg His Pro Thr Met Gly Ser Val Phe Ile Gly Arg  
195 340 345 350  
197 Leu Ile Glu His Met Gln Glu Tyr Ala Cys Ser Cys Asp Val Glu Glu  
198 355 360 365  
200 Ile Phe Arg Lys Val Arg Phe Ser Phe Glu Gln Pro Asp Gly Arg Ala  
201 370 375 380  
203 Gln Met Pro Thr Thr Glu Arg Val Thr Leu Thr Arg Cys Phe Tyr Leu  
204 385 390 395 400  
206 Phe Pro Gly His  
211 (2) INFORMATION FOR SEQ ID NO: 3:  
213 (i) SEQUENCE CHARACTERISTICS:  
214 (A) LENGTH: 269 amino acids  
215 (B) TYPE: amino acid  
216 (D) TOPOLOGY: linear  
217 (ii) MOLECULE TYPE: peptide  
219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
221 Met Ala Glu Val Pro Glu Leu Ala Ser Glu Met Met Ala Tyr Tyr Ser  
222 1 5 10 15  
224 Gly Asn Glu Asp Asp Leu Phe Phe Glu Ala Asp Gly Pro Lys Gln Met  
225 20 25 30  
227 Lys Cys Ser Phe Gln Asp Leu Asp Leu Cys Pro Leu Asp Gly Gly Ile  
228 35 40 45  
230 Gln Leu Arg Ile Ser Asp His His Tyr Ser Lys Gly Phe Arg Gln Ala  
231 50 55 60

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233 Ala Ser Val Val Val Ala Met Asp Lys Leu Arg Lys Met Leu Val Pro  
 234 65 70 75 80  
 236 Cys Pro Gln Thr Phe Gln Glu Asn Asp Leu Ser Thr Phe Phe Pro Phe  
 237 85 90 95  
 239 Ile Phe Glu Glu Glu Pro Ile Phe Phe Asp Thr Trp Asp Asn Glu Ala  
 240 100 105 110  
 242 Tyr Val His Asp Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp  
 243 115 120 125  
 245 Ser Gln Gln Lys Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala  
 246 130 135 140  
 248 Leu His Leu Gln Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met  
 249 145 150 155 160  
 251 Ser Phe Val Gln Gly Glu Ser Asn Asp Lys Ile Pro Val Ala Leu  
 252 165 170 175  
 254 Gly Leu Lys Glu Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp  
 255 180 185 190  
 257 Lys Pro Thr Leu Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys  
 258 195 200 205  
 260 Lys Lys Met Glu Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn  
 261 210 215 220  
 263 Lys Leu Glu Phe Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr  
 264 225 230 235 240  
 266 Ser Gln Ala Glu Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly  
 267 245 250 255  
 268 Gln Asp Ile Thr Asp Phe Thr Met Gln Phe Val Ser Ser  
 269 260 265  
 274 (2) INFORMATION FOR SEQ ID NO: 4:  
 276 (i) SEQUENCE CHARACTERISTICS:  
 277 (A) LENGTH: 18 base pairs  
 278 (B) TYPE: nucleic acid  
 279 (C) STRANDEDNESS: single  
 280 (D) TOPOLOGY: linear  
 W--> 281 (ii) MOLECULE TYPE: DNA  
 283 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 285 TACCGGCTGT TCCAGGAC 18  
 290 (2) INFORMATION FOR SEQ ID NO: 5:  
 292 (i) SEQUENCE CHARACTERISTICS:  
 293 (A) LENGTH: 18 base pairs  
 294 (B) TYPE: nucleic acid  
 295 (C) STRANDEDNESS: single  
 296 (D) TOPOLOGY: linear  
 W--> 297 (ii) MOLECULE TYPE: DNA  
 299 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 301 TACCTATTCT GGGCTCGA 18  
 306 (2) INFORMATION FOR SEQ ID NO: 6:  
 308 (i) SEQUENCE CHARACTERISTICS:  
 309 (A) LENGTH: 17 base pairs  
 310 (B) TYPE: nucleic acid  
 311 (C) STRANDEDNESS: single

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312 (D) TOPOLOGY: linear  
W--> 313 (ii) MOLECULE TYPE: DNA  
315 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
317 TTGGTCGATA CGGGTGT 17  
320 (2) INFORMATION FOR SEQ ID NO: 7:  
322 (i) SEQUENCE CHARACTERISTICS:  
323 (A) LENGTH: 18 base pairs  
324 (B) TYPE: nucleic acid  
325 (C) STRANDEDNESS: single  
326 (D) TOPOLOGY: linear  
W--> 327 (ii) MOLECULE TYPE: DNA  
329 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
331 CACCACACCA AATTCTCA 18  
336 (2) INFORMATION FOR SEQ ID NO: 8:  
338 (i) SEQUENCE CHARACTERISTICS:  
339 (A) LENGTH: 18 base pairs  
340 (B) TYPE: nucleic acid  
341 (C) STRANDEDNESS: single  
342 (D) TOPOLOGY: linear  
W--> 343 (ii) MOLECULE TYPE: DNA  
345 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
347 ATGGAGAAGG GTCCTGTA 18  
352 (2) INFORMATION FOR SEQ ID NO: 9:  
354 (i) SEQUENCE CHARACTERISTICS:  
355 (A) LENGTH: 26 base pairs  
356 (B) TYPE: nucleic acid  
357 (C) STRANDEDNESS: single  
358 (D) TOPOLOGY: linear  
W--> 359 (ii) MOLECULE TYPE: DNA  
361 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
363 GTCGAATTCA AYCCNGCNAT GCCNAC 26  
368 (2) INFORMATION FOR SEQ ID NO: 10:  
370 (i) SEQUENCE CHARACTERISTICS:  
371 (A) LENGTH: 26 base pairs  
372 (B) TYPE: nucleic acid  
373 (C) STRANDEDNESS: single  
374 (D) TOPOLOGY: linear  
W--> 375 (ii) MOLECULE TYPE: DNA  
377 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
379 GTCTCTAGAA GYTTNACRTT NCCYTC 26  
384 (2) INFORMATION FOR SEQ ID NO: 11:  
386 (i) SEQUENCE CHARACTERISTICS:  
387 (A) LENGTH: 43 base pairs  
388 (B) TYPE: nucleic acid  
389 (C) STRANDEDNESS: single  
390 (D) TOPOLOGY: linear  
W--> 391 (ii) MOLECULE TYPE: DNA  
393 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
395 ATATCGGTAC CGCCTCCAGC ATGCCTCCGG CAATGCCAC ATC 43

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/670,106

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Input Set : N:\Crf3\RULE60\09670106.txt  
Output Set: N:\CRF3\05142001\I670106.raw

L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:281 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4  
L:297 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5  
L:313 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6  
L:327 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7  
L:343 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8  
L:359 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9  
L:375 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10  
L:391 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11  
L:407 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12  
L:476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16